

Ernesto Igartua<sup>1</sup>, Bruno Contreras-Moreira<sup>1,2</sup>, Jorge Loscos<sup>1</sup>, María Pilar Gracia<sup>1</sup>, Ana M Casas<sup>1</sup>

<sup>1</sup> Estación Experimental de Aula Dei-CSIC (EEAD-CSIC), Avda Montañana 1005, 50059 Zaragoza, España; <sup>2</sup>Fundación ARAID, Zaragoza, Spain

IBGS 2016  
12<sup>th</sup> International Barley Genetics Symposium

## INTRODUCTION

The barley ortholog of *FLOWERING LOCUS T*, *HvFT1*, also called *VrnH3*, is the main integrator of the photoperiod and vernalization signals leading to the transition from the vegetative to the reproductive stage. Results gathered by several groups over the last years have repeatedly identified QTL for flowering time at the region of this locus. This communication updates and summarizes on the richness of polymorphisms found at this gene, and their associated phenotypic effects.

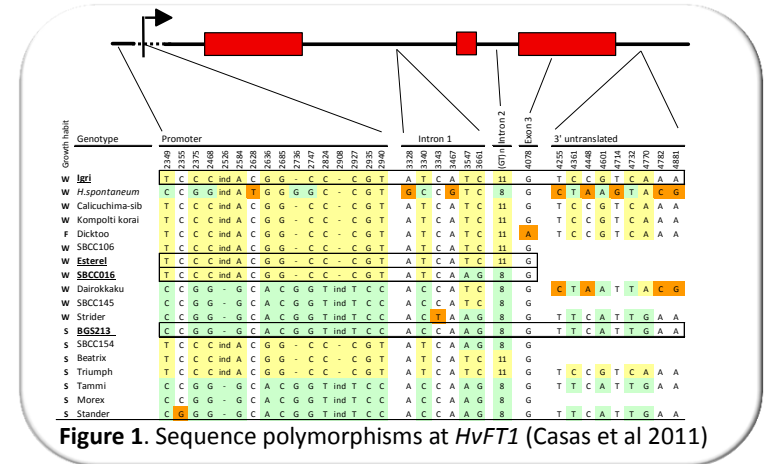


Figure 1. Sequence polymorphisms at *HvFT1* (Casas et al 2011)

## RESULTS

***HvFT1* polymorphisms and effects.** These have been found first at the first intron (Yan et al. 2006), at the promoter (Casas et al. 2011, Figure 1) and also as gene copy number variation (Nitcher et al. 2013). QTL in the *HvFT1* region in biparental crosses with all these types of polymorphisms have been reported (Table 1), reflecting ample phenotypic variation available for plant breeders to choose from.

In some crosses, the QTL at the *HvFT1* region has shown significant interaction with other flowering time QTL (some representing major genes). Therefore, management of *HvFT1* alleles in breeding programs must take into account the possibility of interactions.

| Population        | Field trials               | 1st intron | Promoter      | CNV           | Effect (early parent) | Interactions                 | Ref.                        |
|-------------------|----------------------------|------------|---------------|---------------|-----------------------|------------------------------|-----------------------------|
| Beka x Logan      | 7, fall and spring sowings | –          | Late vs Early | 2 vs 1 copies | 2.8 days (Logan)      | QTL in HvCEN, HvELF3 regions | unpublished                 |
| Beka x Mogador    | 6, fall and winter sowings | –          | –             | 2 vs 1 copies | 2.2 days (Beka)       | No                           | Cuesta-Marcos et al. 2008   |
| Henni x Meltan    | 4, fall sowings            | –          | Late vs Early | –             | 1.5 days (Meltan)     | Not tested                   | Borraàs-Gelonch et al. 2010 |
| SBCC154 x Beatrix | 1, fall sowing             | AG vs TC   | –             | 4 vs 1 copies | 2.5 days (Beatrix)    | No                           | Loscos et al. 2014          |
| SBCC145 x Beatrix | 2, fall and winter sowings | –          | Early vs late | –             | 4.7 days (SBCC145)    | QTL at PpdH1 region          | Ponce-Molina et al. 2012    |
| SBCC016 x Esterel | 2, fall and winter sowings | AG vs TC   | –             | –             | 7.4 days (SBCC016)    | Not tested                   | Casas et al. 2011           |

Table 1. Summary of polymorphisms and effects found in biparental populations

***HvFT1* copy number variation.** There is variation in the number of copies of the *HvFT1* gene, apparently related to growth habit. A large set of winter genotypes, with a functional *VrnH2* allele, has one copy of *VrnH3*, whereas variable number (1-5), was found in also a large set of spring or facultative barleys (without *VrnH2*), as shown in Figure 2.

The dominant *VrnH3* allele, which overrides the vernalization requirement of winter *VrnH1* and *VrnH2* alleles, reported by Nitcher et al. (2013) is found only in Nordic barleys and carries a particular structure of the gene, with one promoter and variable number of transcribed regions.

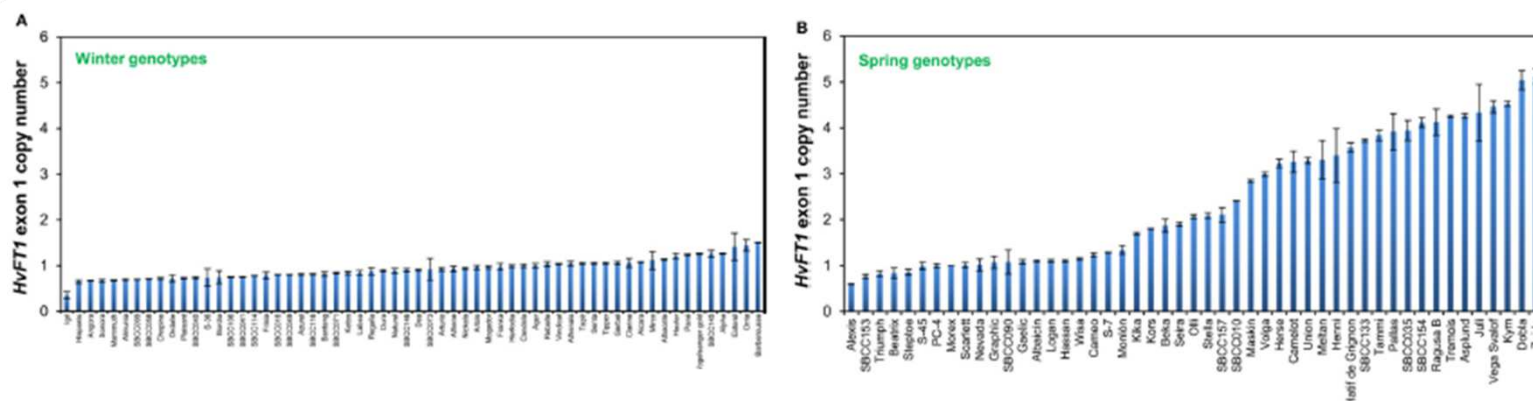


Figure 2. There is copy number variation in *HvFT1*: winter genotypes have one copy whereas spring barleys have a variable number of copies (1-5)

Association studies with geo-referenced barley landraces from Spain revealed:

- Clear association of 1st intron polymorphism with flowering time (Figure 3), and
- Latitudinal variation for the 1st intron polymorphism (Figures 4, 5), with high geographical autocorrelation, at the extreme of the distribution of 7447 markers

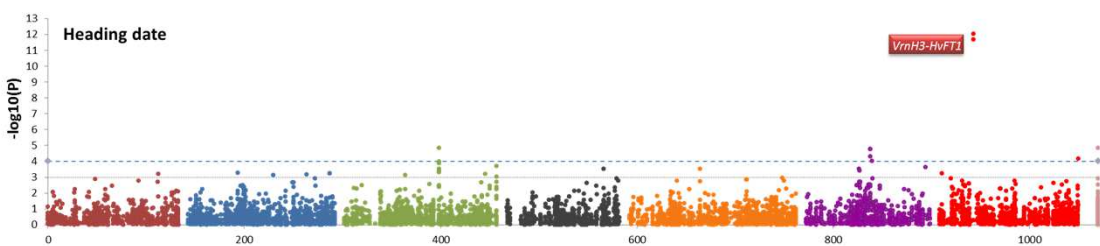


Figure 3. GWAS, K model, for flowering time in the Spanish barley core collection, evaluated at a series of field trials, for over 8000 SNPs.

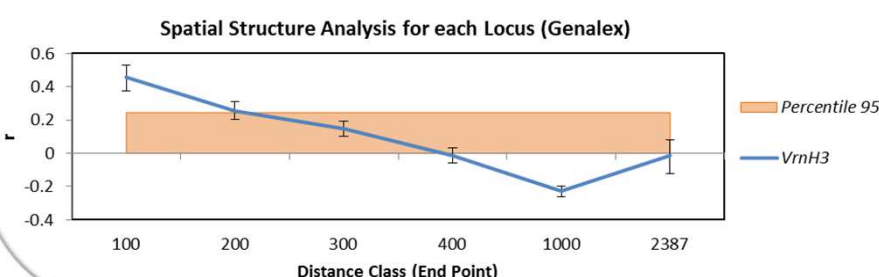


Figure 4. Spatial autocorrelation for *HvFT1*, compared to autocorrelation of 7447 markers distributed over the whole genome.

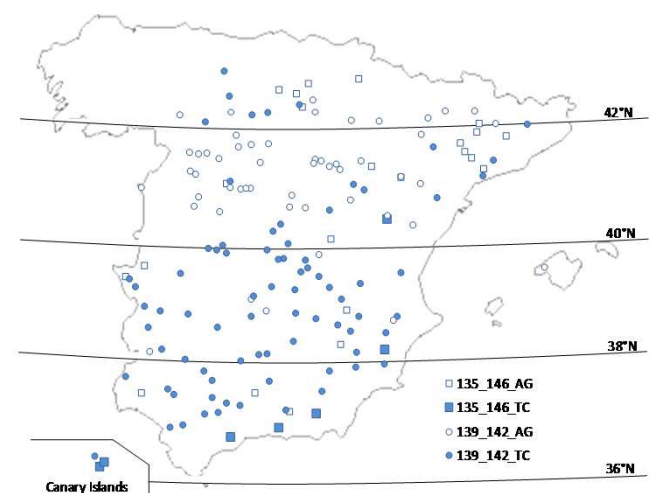


Figure 5. Latitudinal variation for *HvFT1* polymorphism, 1<sup>st</sup> intron, found in the Spanish barley core collection (Casas et al. 2011)